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10	30	50
CAGGGGACATGAGAGGCACACCGAAGACCCACCTCCTGGCCTTCTCCCTCCTCTGCCTCC		
<u>MetArgGlyThrProLysThrHisLeuLeuAlaPheSerLeuLeuCysLeuL</u>		
70	90	110
TCTCAAAGGTGCGTACCCAGCTGTGCCCGACACCATGTACCTGCCCTGGCCACCTCCCC		
<u>euSerLysValArgThrGlnLeuCysProThrProCysThrCysProTrpProProProA</u>		
130	150	170
GATGCCCCGCTGGGAGTACCCCTGGTGCTGGATGGCTGTGGCTGCTGCCGGGTATGTGCAC		
rgCysProLeuGlyValProLeuValLeuAspGlyCysGlyCysCysArgValCysAlaA		
190	210	230
GGCGGCTGGGGGAGCCCTGCGACCAACTCCACGTCTGCGACGCCAGCCAGGGCCTGGTCT		
rgArgLeuGlyGluProCysAspGlnLeuHisValCysAspAlaSerGlnGlyLeuValC		
250	270	290
GCCAGCCCCGGGGCAGGACCCGGTGGCCGGGGGGCCCTGTGCCTCTTGGCAGAGGACGACA		
ysGlnProGlyAlaGlyProGlyGlyArgGlyAlaLeuCysLeuLeuAlaGluAspAspS		
310	330	350
GCAGCTGTGAGGTGAACGGCCGCTGTATCGGGAAGGGGAGACCTTCCAGCCCCACTGCA		
erSerCysGluValAsnGlyArgLeuTyrArgGluGlyGluThrPheGlnProHisCysS		
370	390	410
GCATCCGCTGCCGCTGCGAGGACGGCGGCTTCACCTGCGTGCCGCTGTGCAGCGAGGATG		
erIleArgCysArgCysGluAspGlyGlyPheThrCysValProLeuCysSerGluAspV		
430	450	470
TGCGGCTGCCCAGCTGGGACTGCCCCACCCCAGGAGGGTCGAGGTCCTGGGCAAGTGCT		
alArgLeuProSerTrpAspCysProHisProArgArgValGluValLeuGlyLysCysC		
490	510	530
GCCCTGAGTGGGTGTGCGGCCAAGGAGGGGGACTGGGGACCCAGCCCCTTCCAGCCCAAG		
ysProGluTrpValCysGlyGlnGlyGlyGlyLeuGlyThrGlnProLeuProAlaGlnG		
550	570	590
GACCCAGTTTTCTGGCCTTGTCTCTTCCCTGCCCCCTGGTGTCCCCTGCCAGAATGGA		
lyProGlnPheSerGlyLeuValSerSerLeuProProGlyValProCysProGluTrpS		

FIG. 1A

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610 630 650
GCACGGCCTGGGGACCCTGCTCGACCACCTGTGGGCTGGGCATGGCCACCCGGGTGTCCA
erThrAlaTrpGlyProCysSerThrThrCysGlyLeuGlyMetAlaThrArgValSerA
670 690 710
ACCAGAACCGCTTCTGCCGACTGGAGACCCAGCGCCGCTGTGCCTGTCCAGGCCCTGCC
snGlnAsnArgPheCysArgLeuGluThrGlnArgArgLeuCysLeuSerArgProCysP
730 750 770
CACCTCCAGGGGTCGCAGTCCACAAAACAGTGCCTTCTAGAGCCGGGCTGGGAATGGGG
roProSerArgGlyArgSerProGlnAsnSerAlaPheEnd
790 810 830
ACACGGTGTCCACCATCCCCAGCTGGTGGCCCTGTGCCTGGGCCCTGGGCTGATGGAAGA
850 870 890
TGGTCCGTGCCCAGGCCCTTGGCTGCAGGCAACACTTTAGCTTGGGTCCACCATGCAGAA
910 930 950
CACCAATATTAACACGCTGCCTGGTCTGTCTGGATCCCAGGTATGGCAGAGGTGCAAGA
970 990 1010
CCTAGTCCCCTTTCTCTAACTCACTGCCTAGGAGGCTGGCCAAGGTGTCCAGGGTCCTC
1030 1050 1070
TAGCCCACTCCCTGCCTACACACAGCCTATATCAAACATGCACACGGGCGAGCTTTCT
1090 1110 1130
CTCCGACTTCCCCTGGGCAAGAGATGGGACAAGCAGTCCCTTAATATTGAGGCTGCAGCA
1150 1170 1190
GGTGCTGGGCTGGACTGGCCATTTTTCTGGGGGTAGGATGAAGAGAAGGCACACAGAGAT
1210 1230 1250
TCTGGATCTCCTGCTGCCTTTTCTGGAGTTTGTAATAATTGTTCTGAATACAAGCCTATG
1270
CGTGAAAAAAAAAAAAAAAAAAAAA

FIG.1B

1 50

CTGF-1aa MTAASMGpVR VAFVLLALC SRPAV.GQNC SGPCRCpDEP APRCPAGVSL
 CTGF-3aaMRGTPK THLLAFSLLC LLSKVRTQLC PTPCTCP.WP PPRCPLGVPL

51 100

CTGF-1aa VLDGCGCCRV CAKQLGELCT ERDPCDPHKG LFCDFGSPAN RKIGVC.TAK
 CTGF-3aa VLDGCGCCRV CARRLGEPD QLHVCDASQG LVCQPGAGPG GRGALCLLAE

101 150

CTGF-1aa DGAPCIFGGT VYRSGESFQS SCKYQCTCLD GAVGCMPLCS MDVRLPSPDC
 CTGF-3aa DDSSCEVNGR LYREGETFQP HCSIRCRCD GGFTCVPLCS EDVRLPSWDC

151 200

CTGF-1aa PFPRRVKLPG KCCEEWVCDE PKDQTVVGPA LAAYRLEDTF GPDPTMIRAN
 CTGF-3aa PHPRRVEVLG KCCPEWVCGQ GGGLGTQPLP AQGPQFSGLV SSLPPGVP..

201 250

CTGF-1aa CLVQTTEWSA CSKTCGMGIS TRVTNDNASC RLEKQSRLCM VRPCEADLEE
 CTGF-3aa CPEWSTAWGP CSTTCGLGMA TRVSNQNRFC RLETQRRCL SRPCPPSRGR

251 300

CTGF-1aa NIKKGKKCIR TPKISKPIKF ELSGCTSMKT YRAKFCGVCT DGRCTPHRT
 CTGF-3aa SPQNSAF... ..

301 350

CTGF-1aa TTLPVEFKCP DGEVMKKNNM FIKTCACHYN CPGDNDIFES LYRKMVGDM
 CTGF-3aa

351

CTGF-1aa A
 CTGF-3aa .

FIG.2

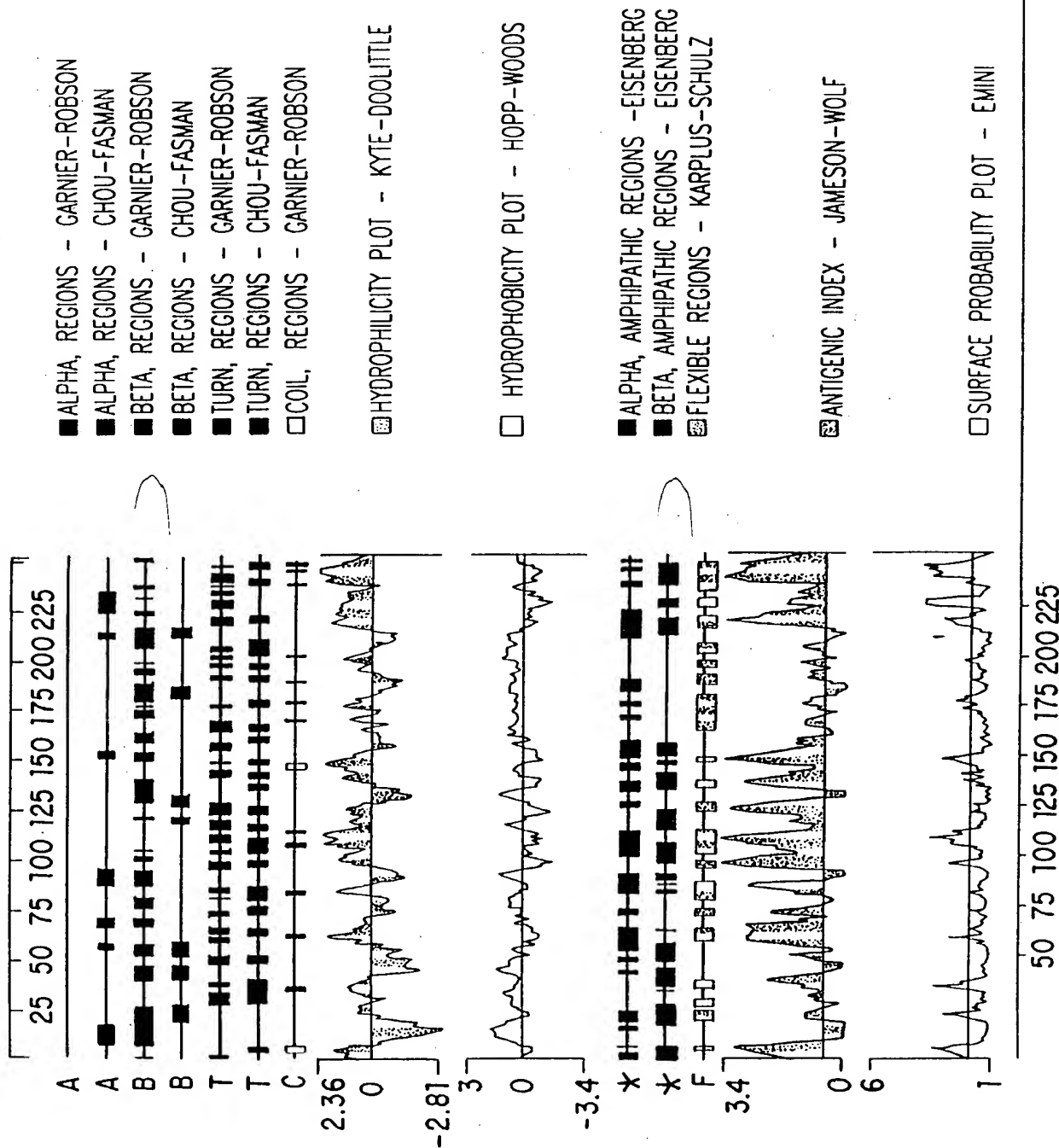


FIG.3